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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Little, Andrew  
Lamparski, Henry  
Schuur, Eric  
Henderson, Daniel

(ii) TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS EXPRESSING ALPHA-FETOPROTEIN AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:  
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(E) COUNTRY: USA  
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/509,591  
(B) FILING DATE: 02-JUN-2000  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/US98/04084  
(B) FILING DATE: 03-MAR-1998

(viii) ATTORNEY/AGENT INFORMATION:  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 822 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCATTGCTGT GAACTCTGTA CTTAGGACTA AACTTGAGC AATAACACAC ATAGATTGAG	60
GATTGTTGC TGTTAGCATA CAAACTCTGG TTCAAAGCTC CTCTTATTG CTTGTCTTGG	120
AAAATTGCT GTTCTTCATG GTTCTCTT TCACTGCTAT CTATTTCT CAACCACTCA	180
CATGGCTACA ATAACGTCT GCAAGCTTAT GATTCCAAA TATCTATCTC TAGCCTCAAT	240
CTTGTTCAG AAGATAAAAAA GTAGTATTCA AATGCACATC AACGTCTCCA CTTGGAGGGC	300
TTAAAGACGT TTCAACATAC AAACCAGGGGA GTTTGCCTG GAATGTTCC TAAAATGTGT	360
CCTGTAGCAC ATAGGGTCCT CTTGTTCTT AAAATCTAAT TACTTTAGC CCAGTGCTCA	420
TCCCCACCTAT GGGGAGATGA GAGTGAAAAG GGAGCCTGAT TAATAATTAC ACTAAGTCAA	480
TAGGCATAGA GCCAGGACTG TTTGGTAAA CTGGTCACTT TATCTTAAAC TAAATATATC	540
CAAAAATGAA CATGTACTTA GTTACTAAGT CTTGACTTT ATCTCATTCA TACCACTCAG	600
CTTTATCCAG GCCACTTATG AGCTCTGTGT CCTTGAACAT AAAATACAAA TAACCGCTAT	660
GCTGTTAATT ATTGGCAAAT GTCCCATTAA CAACTAAGG AAATACCATA AAGTAACAGA	720
TATACCAACA AAAGGTTACT AGTTAACAGG CATTGCCTGA AAAGAGTATA AAAGAATTTC	780
AGCATGATT TCCATATTGT GCTTCCACCA CTGCCAATAA CA	822

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCTTAG AAATATGGGG GTAGGGGTGG TGGTGGTAAT TCTGTTTCA CCCCATAGGT	60
GAGATAAGCA TTGGGTTAAA TGTGTTTCA CACACACATC ACATTCATA AGAATTAAGG	120
AACAGACTAT GGGCTGGAGG ACTTTGAGGA TGTCTGTCTC ATAACACTTG GGTTGTATCT	180
GTTCTATGGG GCTGTTTTA AGCTTGGCAA CTTGCAACAG GGTTCACTGA CTTTCTCCCC	240
AAGCCCAAGG TACTGTCCTC TTTCATATC TGTTTGGGG CCTCTGGGGC TTGAATATCT	300
GAGAAAATAT AAACATTTCA ATAATGTTCT GTGGTGAGAT GAGTATGAGA GATGTGTAT	360
TCATTTGTAT CAATGAATGA ATGAGGACAA TTAGTGTATA AATCCTTAGT ACAACAATCT	420
GAGGGTAGGG GTGGTACTAT TCAATTCTA TTTATAAAGA TACTTATTTC TATTTATTAA	480
TGCTTGTGAC AAATGTTTG TTCGGGACCA CAGGAATCAC AAAGATGAGT CTTTGAATT	540

AAGAAGTTAA TGGTCCAGGA ATAATTACAT AGCTTACAAA TGACTATGAT ATACCATCAA	600
ACAAGAGGTT CCATGAGAAA ATAATCTGAA AGGTTAATA AGTTGTCAAA GGTGAGAGGG	660
CTCTTCTCTA GCTAGAGACT AATCAGAAAT ACATTCAGGG ATAATTATTT GAATAGACCT	720
TAAGGGTTGG GTACATTTG TTCAAGCATT GATGGAGAAG GAGAGTGAAT ATTTGAAAAC	780
ATTTCAACT AACCAACCAC CCAATCCAAC AAACAAAAAA TGAAAAGAAT CTCAGAAACA	840
GTGAGATAAG AGAAGGAATT TTCTCACAAAC CCACACGTAT AGCTCAACTG CTCTGAAGAA	900
GTATATATCT AATATTTAAC ACTAACATCA TGCTAATAAT GATAATAATT ACTGTCATTT	960
TTAATGTCT ATAAGTACCA GGCATTAGA AGATATTATT CCATTATAT ATCAAAATAA	1020
ACTTGAGGGG ATAGATCATT TTCATGATAT ATGAGAAAAA TTAAAAACAG ATTGAATTAT	1080
TTGCCTGTCA TACAGCTAAT AATTGACCAT AAGACAATT A GATTAAATT AGTTTGAAAT	1140
CTTTCTAATA CCAAAGTTCA GTTTACTGTT CCATGTTGCT TCTGAGTGGC TTCACAGACT	1200
TATGAAAAAG TAAACGGAAT CAGAATTACA TCAATGCAA AGCATTGCTG TGAACCTGT	1260
ACTTAGGACT AAACTTTGAG CAATAACACA CATAGATTGA GGATTGTTG CTGTTAGCAT	1320
ACAAACTCTG GTTCAAAGCT CCTCTTATT GCTTGTCTTG GAAAATTGCG TGTTCTTCAT	1380
GGTTTCTCTT TTCACTGCTA TCTATTTTC TCAACCACTC ACATGGCTAC AATAACTGTC	1440
TGCAAGCTTA TGATTCCCAA ATATCTATCT CTAGCCTCAA TCTTGTCCA GAAGATAAAA	1500
AGTAGTATTC AAATGCACAT CAACGTCTCC ACTTGGAGGG CTTAAAGACG TTTCAACATA	1560
CAAACCGGGG AGTTTGCGCT GGAATGTTTC CTAAAATGTG TCCTGTAGCA CATAGGGTCC	1620
TCTTGTTCCT TAAAATCTAA TTACTTTAG CCCAGTGCTC ATCCCACCTA TGGGGAGATG	1680
AGAGTAAAAA GGGAGCCTGA TTAATAATTAA CACTAAGTCA ATAGGCATAG AGCCAGGACT	1740
GTTTGGGTAA ACTGGTCACT TTATCTTAAA CTAATATAT CCAAAACTGA ACATGTACTT	1800
AGTTACTAAG TCTTGACTT TATCTCATTC ATACCACTCA GCTTATCCA GGCCACTTAT	1860
TTGACAGTAT TATTGCGAAA ACTTCCTAAC TGGTCTCCTT ATCATAGTCT TATCCCCTT	1920
TGAAACAAAAA GAGACAGTTT CAAAATACAA ATATGATTTT TATTAGCTCC CTTTGTGTT	1980
CTATAATAGT CCCAGAAGGA GTTATAAACT CCATTAAAAA AGTCTTGAG ATGTGGCCCT	2040
TGCCAACTTT GCCAGGAATT CCCAATATCT AGTATTTCT ACTATTAAAC TTTGTGCCTC	2100
TTCAAAACTG CATTCTCTCT CATTCCCTAA GTGTGCATTG TTTCCCTTA CCGGTTGGTT	2160
TTTCCACCAC CTTTACATT TTCCTGGAAC ACTATACCCCT CCCTCTTCAT TTGGCCCACC	2220

TCTAATTTC	TTTCAGATCT	CCATGAAGAT	GTTACTTCCT	CCAGGAAGCC	TTATCTGACC	2280
CCTCCAAAGA	TGTCATGAGT	TCCTCTTTTC	ATTCTACTAA	TCACAGCATH	CATCACACCA	2340
TGTTGTGATT	ACTGATACTA	TTGTCTGTTT	CTCTGATTAG	GCAGTAAGCT	CAACAAGAGC	2400
TACATGGTGC	CTGCTCTTG	TTGCTGATTA	TTCCCACCCA	AAAACAGTGC	CTGGAATGCA	2460
GAECTAACAT	TTTATTGAAT	GAATAAATAA	AACCCCATCT	ATCGAGTGCT	ACTTTGTGCA	2520
AGACCCGGTT	CTGAGGCATT	TATATTATT	GATTTATTAA	ATTCTCATT	AACCATGAAG	2580
GAGGTACTAT	CACTATCCTT	ATTTTATAGT	TGATAAAGAT	AAAGCCCAGA	GAAATGAATT	2640
AACTCACCCA	AAGTCATGTA	GCTAAGTGAC	AGGGCAAAAA	TTCAAACCAAG	TTCCCCAACT	2700
TTACGTGATT	AATACTGTGC	TATACTGCCT	CTCTGATCAT	ATGGCATGGA	ATGCAGACAT	2760
CTGCTCCGTA	AGGCAGAATA	TGGAAGGAGA	TTGGAGGATG	ACACAAAACC	AGCATAATAT	2820
CAGAGGAAAA	GTCCAAACAG	GACCTGAAC	GATAGAAAAG	TTGTTACTCC	TGGTGTAGTC	2880
GCATCGACAT	CTTGATGAAC	TGGTGGCTGA	CACAACATAC	ATTGGCTTGA	TGTGTACATA	2940
TTATTGTAG	TTGTGTGTGT	ATTTTATAT	ATATATTGT	AATATTGAAA	TAGTCATAAT	3000
TTACTAAAGG	CCTACCATT	GCCAGGCATT	TTTACATTG	TCCCCTCTAA	TCTTTGATG	3060
AGATGATCAG	ATTGGATTAC	TTGGCCTTGA	AGATGATATA	TCTACATCTA	TATCTATATC	3120
TATATCTATA	TCTATATCTA	TATCTATATC	TATATCTATA	TATGTATATC	AGAAAAGCTG	3180
AAATATGTTT	TGTAAAGTTA	TAAAGATTTC	AGACTTTATA	GAATCTGGGA	TTGCCAAAT	3240
GTAACCCCTT	TCTCTACATT	AAACCCATGT	TGGAACAAAT	ACATTATTAA	TTCATTCTAC	3300
AAATGTTGCT	GAGCCTGGC	TATGAACCAG	ACACTGTGAA	AGCCTTGGG	ATATTTGCC	3360
CATGCTTGGG	CAAGCTTATA	TAGTTGCTT	CATAAAACTC	TATTCAGTT	CTTCATAACT	3420
AATACTTCAT	GACTATTGCT	TTTCAGGTAT	TCCTTCATAA	CAAATACTTT	GGCTTTCATA	3480
TATTTGAGTA	AAGTCCCCCT	TGAGGAAGAG	TAGAAGAACT	GCACTTTGTA	AATACTATCC	3540
TGGAATCCAA	ACGGATAGAC	AAGGATGGTG	CTACCTCTT	CTGGAGAGTA	CGTGAGCAAG	3600
GCCTGTTTG	TTAACATGTT	CCTTAGGAGA	CAAAACTTAG	GAGAGACACG	CATAGCAGAA	3660
AATGGACAAA	AACTAACAAA	TGAATGGAA	TTGTACTTGA	TTAGCATTGA	AGACCTTGT	3720
TATACTATGA	TAAATGTTG	TATTTGCTGG	AAGTGCTACT	GACGGTAAAC	CCTTTTGTT	3780
TAAATGTGTG	CCCTAGTAGC	TTGCAGTATG	ATCTATTTT	TAAGTACTGT	ACTTAGCTTA	3840
TTTAAAAAATT	TTATGTTAA	AATTGCATAG	TGCTCTTCA	TTGAAGAAGT	TTTGAGAGAG	3900

AGATAGAATT AAATTCACCT ATCTTACCAT CTAGAGAAC CCAATGTTAA AACTTGTTG	3960
TCCATTATTT CTGTCTTTA TTCAACATTT TTTTAGAGG GTGGGAGGAA TACAGAGGAG	4020
GTACAATGAT ACACAAATGA GAGCACTCTC CATGTATTGT TTTGCCTGT TTTCAGTTA	4080
ACAATATATT ATGAGCATAT TTCCATTTCA TTAAATATTC TTCCACAAAG TTATTTGAT	4140
GGCTGTATAT CACCCTACTT TATGAATGTA CCATATTAAT TTATTCCTG GTGTGGGTTA	4200
TTTGATTTA TAATCTTACC TTTAGAATAA TGAAACACCT GTGAAGCTTT AGAAAATACT	4260
GGTGCCTGGG TCTCAACTCC ACAGATTCTG ATTTAACTGG TCTGGGTTAC AGACTAGGCA	4320
TTGGGAATTTC AAAAAGTTCC CCCAGTGATT CTAATGTGTA GCCAAGATCG GGAACCCCTG	4380
TAGACAGGGA TGATAGGAGG TGAGCCACTC TTAGCATCCA TCATTTAGTA TTAACATCAT	4440
CATCTTGAGT TGCTAAGTGA ATGATGCACC TGACCCACTT TATAAAGACA CATGTGCAA	4500
TAAAATTATT ATAGGACTTG GTTTATTAGG GCTTGTGCTC TAAGTTTCT ATGTTAAGCC	4560
ATACATCGCA TACTAAATAC TTTAAATGT ACCTTATTGA CATACTATT AAGTGAAAAG	4620
TGTTTCTGAG CTAAACAATG ACAGCATAAT TATCAAGCAA TGATAATTG AAATGAATT	4680
ATTATTCTGC AACCTAGGGA CAAGTCATCT CTCTGAATT TTTGTACTTT GAGAGTATT	4740
GTTATATTG CAAGATGAAG AGTCTGAATT GGTCAGACAA TGTCTGTGT GCCTGGCATA	4800
TGATAGGCAT TTAATAGTTT TAAAGAATTA ATGTATTTAG ATGAATTGCA TACCAAATCT	4860
GCTGTCTTT CTTTATGGCT TCATTAACCTT AATTTGAGAG AAATTAATTA TTCTGCAACT	4920
TAGGGACAAG TCATGTCTT GAATATTCTG TAGTTGAGG AGAATATTG TTATATTTGC	4980
AAAATAAAAT AAGTTGCAA GTTTTTTTT TCTGCCCAA AGAGCTCTGT GTCCTGAAAC	5040
ATAAAATACA AATAACCGCT ATGCTGTTAA TTATTGGCAA ATGTCCCATT TTCAACCTAA	5100
GGAAATACCA TAAAGTAACA GATATACCA CAAAGGTAA CTAGTTAACCA GGCATTGCCT	5160
GAAAAGAGTA TAAAAGAATT TCAGCATGAT TTTCCATATT GTGCTTCCAC CACTGCCAAT	5220
AACA	5224

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGTCTTCAA GAATTCTCA

19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTCAGTCAC CGGTGTCGGA

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATTCTCTA GACACAGGTG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGACACCG GTGACTGAAA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCCACGGCC GCATTATATA C

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTATATAATG CGGCCGTGGG C

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCAGAAAATC CAGCAGGTAC C

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGACCGGTG CATTGCTGTG AACTCTGTA

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAAGTGGCC TGGATAAAAGC TGAGTGG

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCACCGGTC TTTGTTATTG GCAGTGGT

28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCCAGGCCA CTTATGAGCT CTGTGTCCTT

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TATCGGCCGG CATTGCTGTG AACTCT

26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTACGGCCGC TTTGTTATTG GCAGTG

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCTTAATTA AAAGCAAACC TCACCTCCG

29

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGGAACAAA AGGTGATTAA AAAATCCAG

30

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACCTTTGT TCCACCGCTC TGCTTATTAC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCTTAATTA ACTGTGAAAG GTGGGAGC

28

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGCTCACT TAAGTTCATG TCG

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCAGCCTAGG AAATATGACT ACGTCCG

27

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

G ATG ACC GGC TCA ACC ATC GCG CCC ACA ACG GAC TAT CGC AAC ACC Met Thr Gly Ser Thr Ile Ala Pro Thr Thr Asp Tyr Arg Asn Thr	46
1 5 10 15	
ACT GCT ACC GGA CTA ACA TCT GCC CTA AAT TTA CCC CAA GTT CAT GCC Thr Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala	94
20 25 30	
TTT GTC AAT GAC TGG GCG AGC TTG GAC ATG TGG TGG TTT TCC ATA GCG Phe Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala	142
35 40 45	
CTT ATG TTT GTT TGC CTT ATT ATT ATG TGG CTT ATT TGT TGC CTA AAG Leu Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys	190
50 55 60	
CGC AGA CGC GCC AGA CCC CCC ATC TAT AGG CCT ATC ATT GTG CTC AAC Arg Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn	238
65 70 75	
CCA CAC AAT GAA AAA ATT CAT AGA TTG GAC GGT CTG AAA CCA TGT TCT Pro His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser	286
80 85 90 95	
CTT CTT TTA CAG TAT GAT TAA Leu Leu Leu Gln Tyr Asp	307
100	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Thr Gly Ser Thr Ile Ala Pro Thr Thr Asp Tyr Arg Asn Thr Thr

1

5

10

15

Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala Phe  
20 25 30

Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala Leu  
35 40 45

Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys Arg  
50 55 60

Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn Pro  
65 70 75 80

His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser Leu  
85 90 95

Leu Leu Gln Tyr Asp  
100